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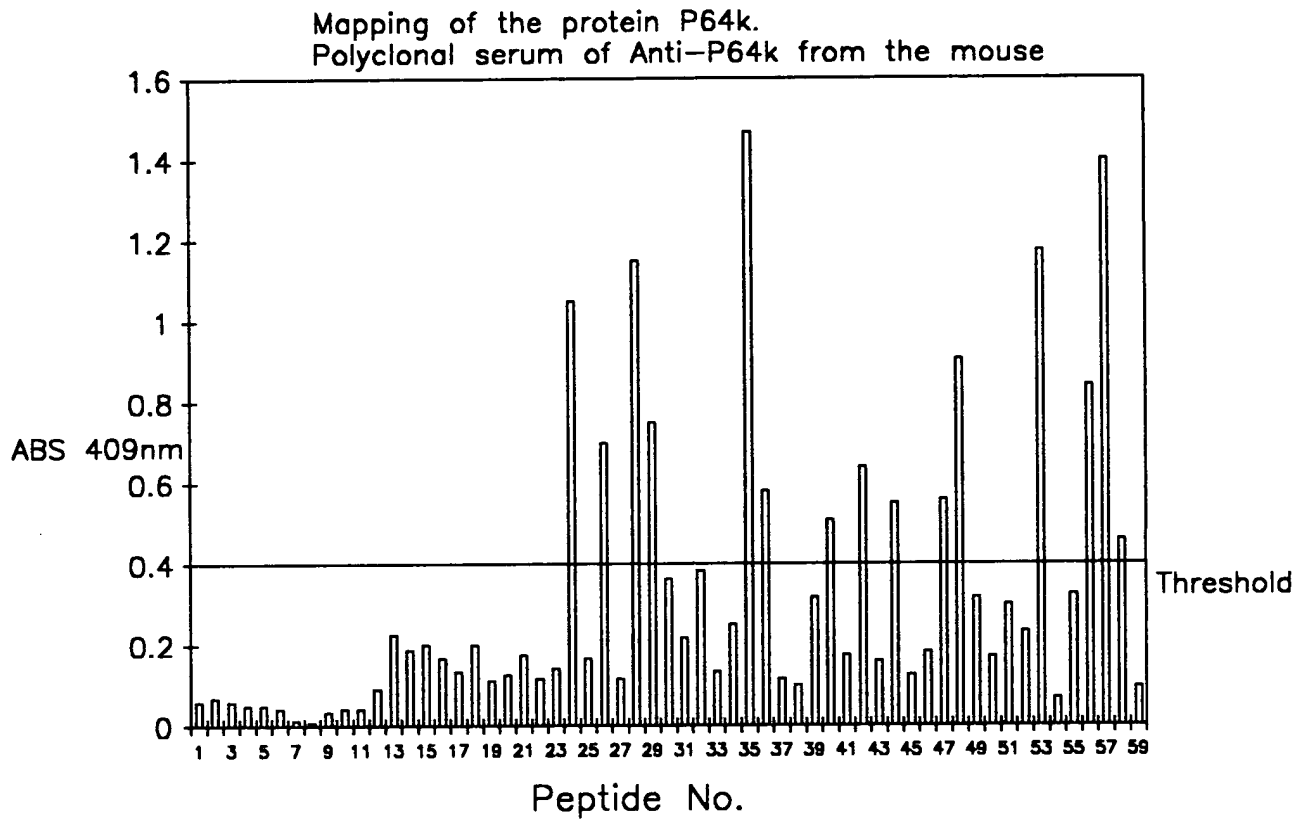
FIG. 1

10	20	30	40	50	60	70
ATGCTAGATA	AAAGAATGGC	TTTAGTTGAA	TTGAAAGTGC	CCGACATTGG	CGGACACGAA	AATGTAGATA
80	90	100	110	120	130	140
TTATCGCGGT	TGAAGTAAAC	GTGGGCGACA	CTATTGCTGT	GGACGATACC	CTGATTACTT	TGGAAACCGA
150	160	170	180	190	200	210
TAAAGCGACT	ATGGACGTAC	CTGCTGAAGT	TGCAGGCGTA	GTCAAAGAAG	TTAAAGTTAA	AGTCGGCGAC
220	230	240	250	260	270	280
AAAATCTCTG	AAGGTGGTTT	GATTGTCGTC	GTTGAAGCTG	AAGGCACGGC	AGCCGCTCCT	AAAGCCGAAG
290	300	310	320	330	340	350
CGGCTGCCGC	CCCGGCGCAA	GAAGCCCCTA	AAGCTGCCGC	TCCTGCTCCG	CAAGCCGCGC	AATTCGGCGG
360	370	380	390	400	410	420
TTCTGCCGAT	GCCGAGTACG	ACGTGGTCGT	ATTGGGTGGC	GGTCCCGGCG	GTTACTCCGC	TGCATTTGCC
430	440	450	460	470	480	490
GCTGCCGATG	AAGGCTTGAA	AGTCGCCATC	GTCGAACGTT	ACAAAACTTT	GGGCGGCGTT	TGCCTGAACG
500	510	520	530	540	550	560
TCGGCTGTAT	CCCTTCCAAA	GCCTTGTTGC	ACAATGCCGC	CGTTATCGAC	GAAGTGCGCC	ACTTGGCTGC
570	580	590	600	610	620	630
CAACGGTATC	AAATACCCCG	AGCCGGAATC	CGACATCGAT	ATGCTTCGCG	CCTACAAAGA	CGGCGTAGTT
640	650	660	670	680	690	700
TCCCGCCTCA	CGGGCGGTTT	GGCAGGTATG	GCGAAAAGCC	GTAAAGTGGG	CGTTATCCAA	GGCGACGGGC
710	720	730	740	750	760	770
AATTCTTAGA	TCCGCACCAC	TTGGAAGTGT	CGCTGACTGC	CGGCGACGCG	TACGAACAGG	CAGCCCCTAC
780	790	800	810	820	830	840
CGGCGAGAAA	AAAATCGTTG	CCTTCAAAAA	CTGTATCATT	GCAGCAGGCA	GCCGCGTAAC	CAAACGCCT
850	860	870	880	890	900	910
TTCATTCTCG	AAGATCCGCA	CATCATCGAT	TCCAGCGGCG	CATTGGCTCT	GAAAGAAGTA	CCGGGCAAAC
920	930	940	950	960	970	980
TGCTGATTAT	CGGCGGCGGC	ATTATCAGCC	TCGAGATGGG	TACGGTTTAC	AGCACGCTGG	GTTTCGCTTT
990	1000	1010	1020	1030	1040	1050
GGATGTGGTT	GAAATGATGG	ACGGCCTGAT	GCAAGGCGCA	GACCGCGATT	TGGTAAAAGT	ATGGCAAAAA
1060	1070	1080	1090	1100	1110	1120
CAAAACGAAT	ACCGTTTTGA	CAACATTATG	GTCAACACCA	AAACCGTTGC	AGTTGAGCCG	AAAGAAGACG
1130	1140	1150	1160	1170	1180	1190
GCGTTTACGT	TACCTTTGAA	GGCGCGAACG	CGCCTAAAGA	GCCGCAACGC	TACGATGCCG	TATTGGTTGC
1200	1210	1220	1230	1240	1250	1260
CGCCGGCCGC	GCGCCCAACG	GCAAATCAT	CAGCGCGGAA	AAAGCAGGCG	TTGCCGTAAC	CGATCGCGGC
1270	1280	1290	1300	1310	1320	1330
TTCATCGAAG	TGGACAAACA	AATGCGTACC	AATGTGCCGC	ACATCTACGC	CATCGGCGAC	ATCGTCGGTC
1340	1350	1360	1370	1380	1390	1400
AGCCGATGTT	GGCGCACAAA	GCCGTTACAG	AAGGCCACGT	TGCCGCGGAA	AACTGCGCCG	GCCACAAAGC
1410	1420	1430	1440	1450	1460	1470
CTACTTCGAC	GCACGCGTGA	TTCCGGGCGT	TGCCTACACT	TCCCCCGAAG	TGGCGTGGGT	GGGCGAAACC
1480	1490	1500	1510	1520	1530	1540
GAACTGTCCG	CCAAAGCCTC	CGGCCGCAAA	ATCACCAAAG	CCAACCTCCC	GTGGGCGGCT	TCCGGCCGTG
1550	1560	1570	1580	1590	1600	1610
CGATTGCCAA	CGGTTGCGAC	AACGGCTTTA	CCAAGCTGAT	TTTTGATGCC	GAAACCGGCC	GCATCATCGG
1620	1630	1640	1650	1660	1670	1680
CGGCGGCATT	GTCGGTCCGA	ACGGTGCCGA	TATGATCGGC	GAAGTCTGCC	TTGCCATCGA	AATGGGCTGC
1690	1700	1710	1720	1730	1740	1750
GACGCGGCAG	ACATCGGCAA	AACCATCCAC	CCGCACCCGA	CCTTGGGCGA	ATCCATCGGT	ATGGCGGCGG
1760	1770	1780	1790	1797		
AAGTGGCATT	GGGTACTTGT	ACCGACCTGC	CTCCGCAAAA	GAAAAAA		

CGCTTTACGT

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DEFTSMAN		

FIG. 2



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CHAFTSMAN		

FIG. 5

Sequences producing High-scoring Segment Pairs:

	Smallest Poisson
High	Probability
Score	P(N) N

KPY1_HUMAN	PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40).	51	0.98	1
KPY1_RAT	PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40).	51	0.98	1
KPY2_HUMAN	PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).	51	0.98	1
KPY2_RAT	PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).	51	0.98	1

>KPY1_HUMAN PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40) (CYTOSOLIC THYROID HORMONE-BINDING PROTEIN)
Length = 530

Query: 29 VNVGDTIAVDDTLITLTL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY1_RAT PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY2_HUMAN PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY2_RAT PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DATE		

FIG. 8

M V D K R M A L V E L K V P D I G G H
 ATG GTA GAT AAA AGA ATG GCT TTA GTT GAA TTG AAA GTG CCC GAC ATT GGC GGA CAC
 E N V D I I A V E V N V G D T I A V D
 AA AAT GTA GAT ATT ATC GCG GTT GAA GTA AAC GTG GGC GAC ACT ATT GCT GTG GAC
 D T L I T L D L D S R G I R I G P G R
 GAT ACC CTG ATT ACT TTG GAT CTA GAC TCG AGA GGC ATT CGT ATC GGC CCA GGT CGC
 A I L A T A G G G A R Q S T P I G L G
 GCA ATT TTA GCA ACA GCT GGC GGT GGC GCA CGT CAA TCT ACC CCT ATT GGT TTA GGT
 G A L Y T T A G G G A R K S I T K G P
 CAG GCT CTG TAT ACG ACT GCC GGC GGT GGT GCG CGC AAA AGT ATC ACC AAG GGT CCA
 G R V I Y A T A G G G A R K R I H I G
 GGC CGC GTC ATT TAC GCC ACC GCG GGC GGC GGT GCC CGT AAG CGT ATC CAC ATT GGC
 P G R A F Y T T A G G G A R K R I T M
 CCA GGC CGT GCA TTC TAT ACT ACA GCA GGT GGT GGC GCA CGT AAA CGC ATC ACT ATG
 G P G R V Y Y T T A G G G A S I R I Q
 GGT CCT GGT CGC GTC TAT TAC ACG ACC GCT GGC GGC GGT GCT AGC ATT CGC ATC CAA
 R G P G R A F V T I *
 CGC GGC CCT GGT CGT GCA TTT GTG ACC ATA TGA

000720 52527950

FIG. 10A

Gene	Stabilizer	Plasmid	Culture medium	% of expression
<i>porA</i>	hIL2-58	pILM-28	M9	32
	P64k-47	pM-82	M9	34
<i>opc</i>	hIL2-58	pILM-29	M9	25
	P64k-47	pM-80	M9	20
TAB	hIL2-22	pTAB4	LB	5
	P64k-47	pTAB4	LB	10

FIG. 10B

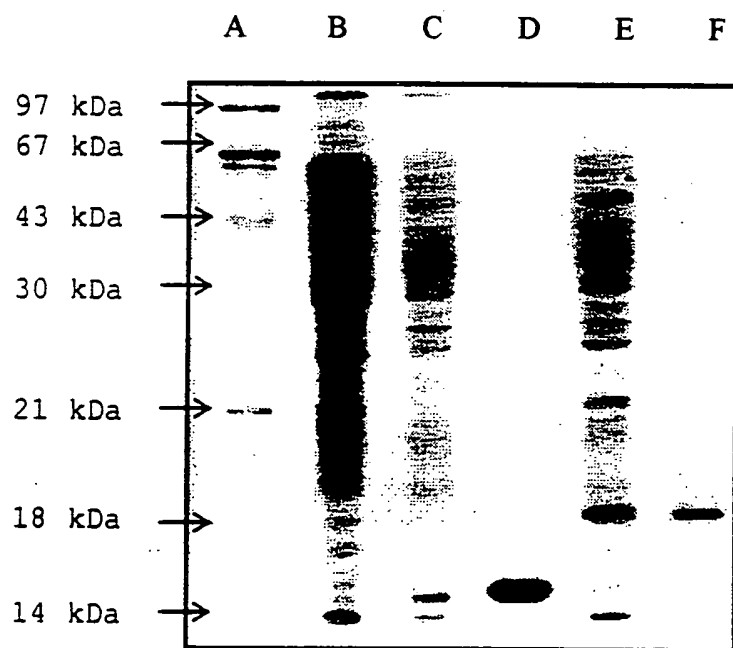
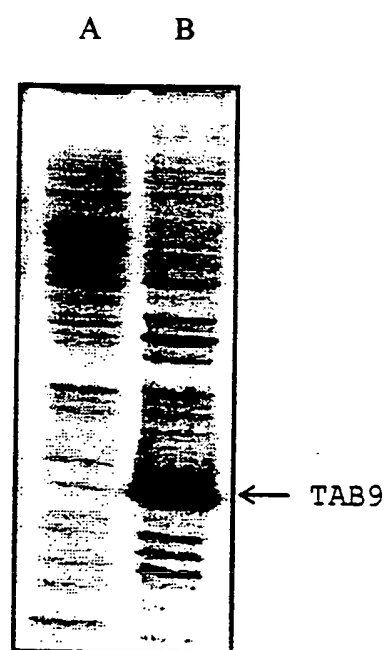
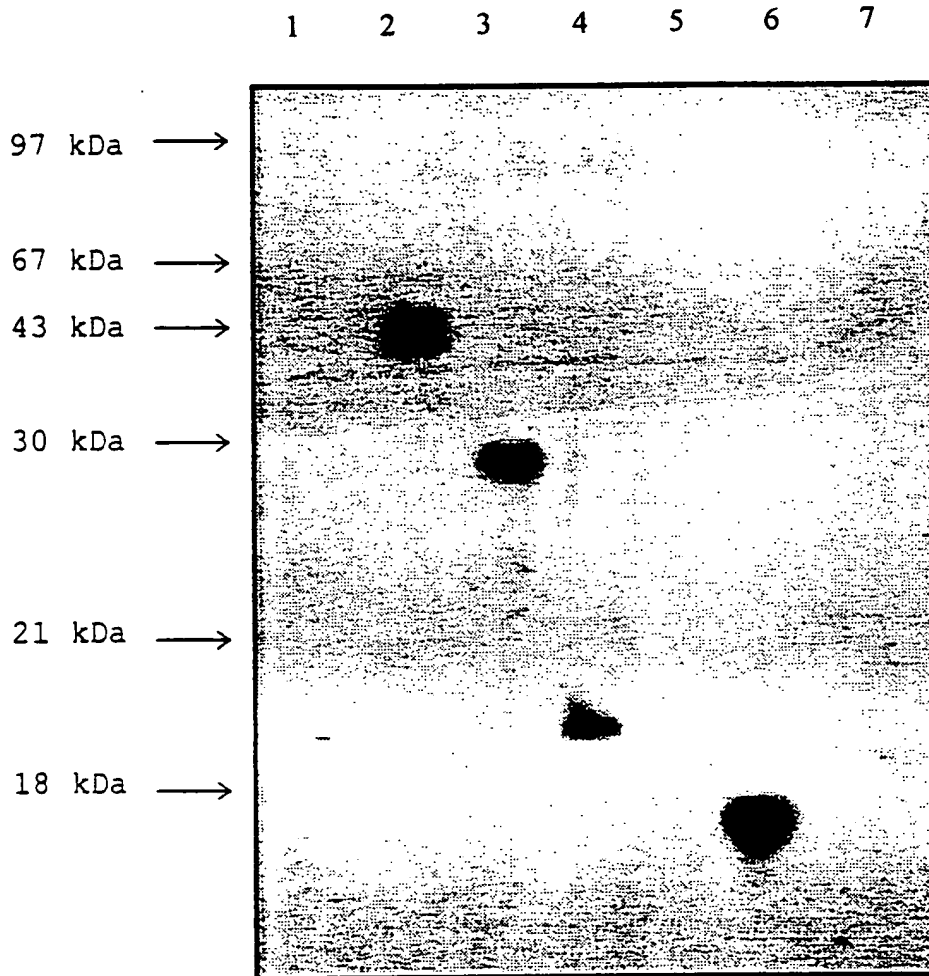


FIG. 10C



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 11



000120-6662960

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 12

	TAB 4				TAB 9			
RABBIT#	12166	5725	5340	2310	1	2	3	10
TAB	20480	10240	10240	81920	20480	20480	51200	51200
	0	0	0	0	0	0		
LR150	<100	<100	<100	6400	400	<100	800	<100
JY1	200	<100	<100	12800	1600	6400	3200	<100
RF	6400	<100	3200	800	<100	200	3200	800
MN	200	<100	<100	1600	1600	3200	6400	<100
BRVA	<100	6400	400	3200	800	400	6400	1600
IIIB	<100	<100	<100	<100	800	<100	800	<100
GM	1820				1416			
R%	45.8%				75%			

000720-62521350